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ALIGNED SEQUENCES

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Homology 948 948 858 678		tatgogggoga:	rtgcccagcttatgg.agg.atg.atg.agtg.at.g ggg.tt.g	gtaactgtgaattgg	atgaagggcctaaatccttg .ca .ca .ca
(2398 bps) (2398 bps) (2398 bps) (2179 bps) (2179 bps) (2433 bps) (2430 bps) (2426 bps)	end Gap 3	gttcttgttatatt	constant de consta	rtacgaaacttgtaactgtgaattggccatcg c.c	ttgaggttactaat .a.aa.aga.a.gaaga.aga.a
2603 2445 2399 2181 2475 5088	3; Exte	aagaaaag aaaaa ttt	gccgtgga .tgat	ctgatggt .c .c .c	ccgaact g ttagct. gttagcg.
206 - 48 - 2 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2	Open Gap	acacccaaagagcaagaaa 	rgaagcgc g aa.gaa.gaa.gaa	cacctttctc. ttctc. t.ac. ggg	ggcaaagaagtaaccgaac .t.gt.gtg. .t.gt.gtg. .t.gc.t.g.
Cslseq Kukkaseq Ds4seq 2301SEQ 390seq H. felis comp H. pylori com	Global DNA Mismatch 1; Op	gtgaaactcacacccaaagagcaagaaaa w a a a a a a c a c a c a c a c a c a c a c a c a c a c a c a c a a c a a a a a a a a a a a a a	gcccatattatggacgaagcgcgcgtgg gcccatattatggacgaagcgcgcgtgg gcccgtgg gg.g.g.g.g.g.g.g.g.g.g.g.g.g.g.g.g	0 + + · · · - ·	ctcaatgca cg a.t.cc
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Figure 1a (1)

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Figure 1a (2)

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Figure 1a (3)

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Figure 1a (4)

ALIGNED SEQUENCES	Le: ureXCS1	Global Protein Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N	vkltpkeqekfllyyagevarkrkaeglklnqpeaiayisahimdearrgkktvaqlmeecmhflkkdevmpgvgnmvpdlgveatfpdgtklvtvnwpiepdehfkagevkfgcdkdie
66.	Reference molecule: Sequence 2: Sequence 3: Sequence 4: Sequence 5: Sequence 6: Sequence 7: Sequence 7:	Alignment type: Parameters:	
11/15/99	Refere	Alignment t Parameters:	urexCS1 urexbs4 urex2301 urex2301 urex390 A felis A pylori A heilman urexCS1 urexCS1 urexCS1 urexCS301 urexCS04 urexCS04 urexCS1

Figure 1b

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ALIGNED SEQUENCES

ureYCS1 1 - 568 (568 aa) Homology	ureYkuka1 - 568 (568 aa)99%ureYDS41 - 568 (568 aa)98%ureY23011 - 568 (568 aa)99%ureY33011 - 496 (496 aa)86%B felis1 - 569 (569 aa)73%B pylori1 - 569 (569 aa)73%B heilman1 - 568 (568 aa)74%	Global Protein Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N	mkmkkq-eyvntygptkgdkvrlgdtdlwaevehdyttygeelkfgagktiregmgqsnspdentldlvitnamiidytgiykadigikngkihgigkagnkdmqdgvsphmvvg t t -		10 ydvqvcihtdtvneagyvddtlnamngraihayhiegaggnspdvitmagelnilpssttptipytintvaehldmlmtchhldkriredlqfsqsrlrpgsiaaedvlhdmgviamts	60) sdsgamgrageviprtwqtadknkkefgklpedgkdndnfrikryiskytinpalthgvseyigsveegkiadlvvwnpaffgvkpkivikggmvvfsemgdsnasvptpqpvyyremfg 60) 60) 60) 60) 61) 7
			aaaaaaaaa	120) 120) 120) 120) 120) 121) 121)	240) 240) 240) 240) 241) 241)	360) 360) 360) 360) 360) 361) 361)
Reference molecule:	Sequence Sequence Sequence Sequence Sequence Sequence	Alignment type: Parameters:	ureYCS1 ureYbka ureYDS4 ureY2301 ureY2300 b felis B pylori B heilman	ureYCS1 ureYkuka ureYDS4 ureY2301 ureY2300 ureY390 b felis b pylori B beilman	ureYCS1 ureYkuka ureYSA4 ureY2301 ureY390 B felis B pylori B heilman	ureYCS1 ureYkuka ureYS34 ureY3301 ureY390 B felis B pylori B heilman

Figure 1c (1)

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ureYCS1 ureYbS4 ureY2301 ureY390 B felis B pylori B heilman

Figure 1c (2)

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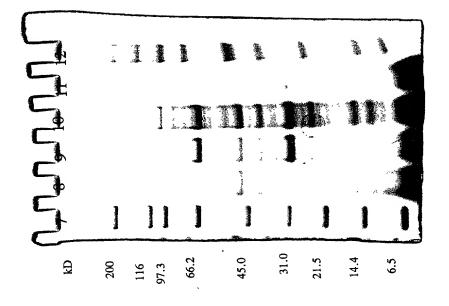


Figure 2

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